



OIPE

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/079,699

DATE: 03/08/2002

TIME: 15:23:36

Input Set : A:\2104seq.txt

Output Set: N:\CRF3\03082002\J079699.raw

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4 <110> APPLICANT: Nicholette, Charles A.
6 <120> TITLE OF INVENTION: PAR-3 COMPOUNDS FOR THERAPY AND DIAGNOSIS AND METHODS FOR
USING SAME
8 <130> FILE REFERENCE: GZ 2104.20
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/079,699
C--> 11 <141> CURRENT FILING DATE: 2002-02-19
13 <150> PRIOR APPLICATION NUMBER: 60/226,243
14 <151> PRIOR FILING DATE: 2000-08-17
16 <160> NUMBER OF SEQ ID NOS: 12
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 3801
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <400> SEQUENCE: 1
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27 atgaaagtgt tcagcctcat ccagcaggcg gtgaccogct accggaaggc catcgccaag 120
28 gatccaaact actggataca ggtgcatcgc ttggaacatg gagatggagg aatactagac 180
29 cttgatgaca ttctttgtga tgtagcagac gataaagaca gactggtagc agtgtttgat 240
30 gagcaggatc cacatcacgg aggtgatggc accagtgccg gtccacaggg taccagagc 300
31 ccagagatat ttggtagtga gcttggcacc aacaatgtct cagcctttca gccttaccac 360
32 gcaacaagtg aaattgaggt cacaccttca gtccttcgag caaatatgcc tcttcattgt 420
33 cgacgcagta gtgaccagc tctaattggc ctctccactt ctgtcagtga tagtaatttt 480
34 tcctctgaag agccttcaag gaaaaatccc acacgctggg caacaacagc tggcttcttc 540
35 aagcagaaca ctgctggggag tcttaaaacc tgcgacagga aggatgagga tgggacagaa 600
36 gaggataaca gtcgtgttga acctgttgga catgctgaca cgggttttga gcatataccc 660
37 aacttttctc tggatgatat ggtaaagctc gtagaagtcc ccaacgatgg agggcctctg 720
38 ggaatccatg tagtgctctt cagtgtctga ggcggcagaa ccttgggggt attagtaaaa 780
39 cgattggaga aaggtggtaa agctgaacat gaaaatcttt ttcttgagaa tgattgcatt 840
40 gtcaggatta atgatggcga ccttcgaaat agaagatttg aacaagcaca acatatgttt 900
41 cgccaagcca tgcgtacacc catcatttgg ttccatgtgg ttctgcagc aaataaagag 960
42 cagtatgaac aactatccca aagtgagaag aacaattact attcaagcg ttttagcctt 1020
43 gacagccagt atattgacaa caggagtgtg aacagtgcag ggcttcacac ggtgcagaga 1080
44 gcaccccgac tgaaccaccc gcctgagcag atagactctc actcaagact acctcatagc 1140
45 gcacaccctc cgggaaaacc accatccgct ccagcctcgg cacttcagaa tgtatttagt 1200
46 acgactgtaa gcagtggtaa taacaccaa aaaataggca agaggcttaa tatccagctt 1260
47 aagaaaggta cagaagggtt gggattcagc atcacttcca gagatgtaac aatagggtggc 1320
48 tcagctccaa tctatgtgaa aaacattctc ccccgggggg cggccattca ggatggccga 1380
49 cttaaggcag gagacagact tatagaggta aatggagtag atttagtggg caaatcccaa 1440
50 gaggaagtgt ttctgctgtt gagaagcacc aagatggaag gaaatgtgag ccttctggtc 1500
51 ttctgccagg aagacgcctt ccaccaagg gaactgaaag cagaagatga ggatattgtt 1560
52 cttaacactg atggcaccag ggaatttctg acatttgaag tccacttaa tgattcagga 1620
53 tctgcaggcc ttggtgtcag tgtcaaaggt aaccggtcaa aagagaacca cgcagatttg 1680
54 ggaatcttgc tcaagtccat tattaatgga ggagcagcat cttaagatgg aaggcttcgg 1740

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55 gtgaatgatc aactgatagc agtaaattgga gaatccctgt tgggcaagac aaaccaagat 1800
56 gccatggaaa ccctaagaag gtctatgtct actgaaggca ataaacgagg aatgatccag 1860
57 cttattgttg caaggagaat aagcaagtgc aatgagctga agtcacctgg gagccccct 1920
58 ggacctgagc tgcccattga aacagcgttg gatgatagag aacgaagaat ttcccatcc 1980
59 ctctacagtg ggattgaggg gcttgatgaa tccccaaagca gaaatgctgc cctcagtagg 2040
60 ataattgggtg aataccagct gtcccctaca gtgaatatgc cccaagatga cactgtcatt 2100
61 atagaagatg acaggttgcc agtgcttctt ccacatctct ctgaccagtc ctcttccagc 2160
62 tcccatgatg atgtgggggt tgtgacggca gatgctggta cttgggcca ggctgcaatc 2220
63 agtgattcag ccgactgctc tttgagtcga gatgttgatc cagttcttgc ttttcaacga 2280
64 gaaggatttg gacgtcagat agctgacgag actaaactca atacagtggg tgaccagaaa 2340
65 gcaggttctc ccagcagaga tgtgggtcct tccctgggtc tgaagaagtc aagctcgttg 2400
66 qagagtctgc agaccgcagt tgccgaggtg actttgaatg gggatattcc tttccatcgt 2460
67 ccacggccgc ggataatcag aggcagggga tgcaatgaga gcttcagagc tgccatcgac 2520
68 aaatcttatg ataaacccgc ggtagatgat gatgatgagg gcatggagac cttggaagaa 2580
69 gacacagaag aaagttcaag atcaggggaga gagtctgtat ccacagccag tgatcagcct 2640
70 tcccactctc tggagagaca aatgaatgga aaccaagaga aaggtgataa gactgataga 2700
71 aaaaaggata aaactggaaa agaaaagaag aaagatagag ataaggagaa ggataaaatg 2760
72 aaagccaaga agggaatgct gaagggttg ggagacatgt tcaggtttg caaacatcga 2820
73 aaagatgaca agattgagaa aacgggtaaa ataaaaatac aggaatcctt tacatcagaa 2880
74 gaggagagga tacgaatgaa gcaggagcag gagaggattc aagccaaaac tcgagaattt 2940
75 agggaacgac aagctcgaga gcgtgactat gctgaaattc aagattttca tcggacattt 3000
76 ggctgtgatg atgagttaat gtatggggga gtttcttctt atgaaggttc catggctctc 3060
77 aacgctagac ctgagagccc acgagaaggg catatgatgg atgctttgta tgcccaagtc 3120
78 aagaagccgc ggaattccaa accctcacct gtagacagta acagatcaac tcctagcaat 3180
79 catgatcgga tacagcgtct gaggcaagaa tttcagcaag caaagcaaga tgaagatgta 3240
80 gaagatcgtc ggcggaccta tagttttgag caacctggc cgaacgcacg gccggcgacg 3300
81 cagagcgggc gacactcggg gtccgtggag gtgcagatgc agcggcagcg gcaggaggag 3360
82 cgcgagagct cccagcaggc ccagcgcag tacagctctc tgctcggca aagcaggaaa 3420
83 aatgccagct cggctctcca ggactcttgg gagcagaact actccctgg ggaaggcttc 3480
84 cagagtgcc aagagaacct caggtactcc agctaccaag gctccaggaa cggctacctg 3540
85 ggaggacatg gttcaacgc cagggtcag ctggaaactc aggagctcct tcgccaggaa 3600
86 cagaggcgga aggagcagca gatgaagaag cagcctcctt ccgaggggccc cagcaactat 3660
87 gactcgtata agaaagtcca ggacccccagt tacgccccct ccaaggggccc ctccggcaa 3720
88 gatgtgcccc cctccccctt tcaggttgcg aggtgaaca gacttcagac tcctgagaaa 3780
89 gggaggccct tctattcctg a 3801

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91 <210> SEQ ID NO: 2

92 <211> LENGTH: 1266

93 <212> TYPE: PRT

94 <213> ORGANISM: Homo sapiens

96 <400> SEQUENCE: 2

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97 Met Lys Val Thr Val Cys Phe Gly Arg Thr Arg Val Val Val Pro Cys
98 1 5 10 15
99 Gly Asp Gly His Met Lys Val Phe Ser Leu Ile Gln Gln Ala Val Thr
100 20 25 30
101 Arg Tyr Arg Lys Ala Ile Ala Lys Asp Pro Asn Tyr Trp Ile Gln Val
102 35 40 45
103 His Arg Leu Glu His Gly Asp Gly Gly Ile Leu Asp Leu Asp Asp Ile
104 50 55 60
105 Leu Cys Asp Val Ala Asp Asp Lys Asp Arg Leu Val Ala Val Phe Asp

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106	65					70				75					80	
107	Glu	Gln	Asp	Pro	His	His	Gly	Gly	Asp	Gly	Thr	Ser	Ala	Ser	Ser	Thr
108					85					90					95	
109	Gly	Thr	Gln	Ser	Pro	Glu	Ile	Phe	Gly	Ser	Glu	Leu	Gly	Thr	Asn	Asn
110				100					105						110	
111	Val	Ser	Ala	Phe	Gln	Pro	Tyr	Gln	Ala	Thr	Ser	Glu	Ile	Glu	Val	Thr
112				115				120						125		
113	Pro	Ser	Val	Leu	Arg	Ala	Asn	Met	Pro	Leu	His	Val	Arg	Arg	Ser	Ser
114		130					135					140				
115	Asp	Pro	Ala	Leu	Ile	Gly	Leu	Ser	Thr	Ser	Val	Ser	Asp	Ser	Asn	Phe
116	145					150					155					160
117	Ser	Ser	Glu	Glu	Pro	Ser	Arg	Lys	Asn	Pro	Thr	Arg	Trp	Ser	Thr	Thr
118					165					170						175
119	Ala	Gly	Phe	Leu	Lys	Gln	Asn	Thr	Ala	Gly	Ser	Pro	Lys	Thr	Cys	Asp
120				180						185					190	
121	Arg	Lys	Asp	Glu	Asp	Gly	Thr	Glu	Glu	Asp	Asn	Ser	Arg	Val	Glu	Pro
122			195					200						205		
123	Val	Gly	His	Ala	Asp	Thr	Gly	Leu	Glu	His	Ile	Pro	Asn	Phe	Ser	Leu
124		210					215						220			
125	Asp	Asp	Met	Val	Lys	Leu	Val	Glu	Val	Pro	Asn	Asp	Gly	Gly	Pro	Leu
126	225					230					235					240
127	Gly	Ile	His	Val	Val	Pro	Phe	Ser	Ala	Arg	Gly	Gly	Arg	Thr	Leu	Gly
128					245					250					255	
129	Leu	Leu	Val	Lys	Arg	Leu	Glu	Lys	Gly	Gly	Lys	Ala	Glu	His	Glu	Asn
130				260						265					270	
131	Leu	Phe	Arg	Glu	Asn	Asp	Cys	Ile	Val	Arg	Ile	Asn	Asp	Gly	Asp	Leu
132			275						280					285		
133	Arg	Asn	Arg	Arg	Phe	Glu	Gln	Ala	Gln	His	Met	Phe	Arg	Gln	Ala	Met
134		290					295						300			
135	Arg	Thr	Pro	Ile	Ile	Trp	Phe	His	Val	Val	Pro	Ala	Ala	Asn	Lys	Glu
136	305					310					315					320
137	Gln	Tyr	Glu	Gln	Leu	Ser	Gln	Ser	Glu	Lys	Asn	Asn	Tyr	Tyr	Ser	Ser
138				325						330					335	
139	Arg	Phe	Ser	Pro	Asp	Ser	Gln	Tyr	Ile	Asp	Asn	Arg	Ser	Val	Asn	Ser
140				340						345					350	
141	Ala	Gly	Leu	His	Thr	Val	Gln	Arg	Ala	Pro	Arg	Leu	Asn	His	Pro	Pro
142			355					360					365			
143	Glu	Gln	Ile	Asp	Ser	His	Ser	Arg	Leu	Pro	His	Ser	Ala	His	Pro	Ser
144		370					375						380			
145	Gly	Lys	Pro	Pro	Ser	Ala	Pro	Ala	Ser	Ala	Pro	Gln	Asn	Val	Phe	Ser
146	385					390					395					400
147	Thr	Thr	Val	Ser	Ser	Gly	Tyr	Asn	Thr	Lys	Lys	Ile	Gly	Lys	Arg	Leu
148					405					410					415	
149	Asn	Ile	Gln	Leu	Lys	Lys	Gly	Thr	Glu	Gly	Leu	Gly	Phe	Ser	Ile	Thr
150				420						425				430		
151	Ser	Arg	Asp	Val	Thr	Ile	Gly	Gly	Ser	Ala	Pro	Ile	Tyr	Val	Lys	Asn
152			435						440					445		
153	Ile	Leu	Pro	Arg	Gly	Ala	Ala	Ile	Gln	Asp	Gly	Arg	Leu	Lys	Ala	Gly
154		450					455					460				

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155 Asp Arg Leu Ile Glu Val Asn Gly Val Asp Leu Val Gly Lys Ser Gln
156 465                               470                               475                               480
157 Glu Glu Val Val Ser Leu Leu Arg Ser Thr Lys Met Glu Gly Thr Val
158                               485                               490                               495
159 Ser Leu Leu Val Phe Arg Gln Glu Asp Ala Phe His Pro Arg Glu Leu
160                               500                               505                               510
161 Lys Ala Glu Asp Glu Asp Ile Val Leu Thr Pro Asp Gly Thr Arg Glu
162                               515                               520                               525
163 Phe Leu Thr Phe Glu Val Pro Leu Asn Asp Ser Gly Ser Ala Gly Leu
164                               530                               535                               540
165 Gly Val Ser Val Lys Gly Asn Arg Ser Lys Glu Asn His Ala Asp Leu
166 545                               550                               555                               560
167 Gly Ile Phe Val Lys Ser Ile Ile Asn Gly Gly Ala Ala Ser Lys Asp
168                               565                               570                               575
169 Gly Arg Leu Arg Val Asn Asp Gln Leu Ile Ala Val Asn Gly Glu Ser
170                               580                               585                               590
171 Leu Leu Gly Lys Thr Asn Gln Asp Ala Met Glu Thr Leu Arg Arg Ser
172                               595                               600                               605
173 Met Ser Thr Glu Gly Asn Lys Arg Gly Met Ile Gln Leu Ile Val Ala
174                               610                               615                               620
175 Arg Arg Ile Ser Lys Cys Asn Glu Leu Lys Ser Pro Gly Ser Pro Pro
176 625                               630                               635                               640
177 Gly Pro Glu Leu Pro Ile Glu Thr Ala Leu Asp Asp Arg Glu Arg Arg
178                               645                               650                               655
179 Ile Ser His Ser Leu Tyr Ser Gly Ile Glu Gly Leu Asp Glu Ser Pro
180                               660                               665                               670
181 Ser Arg Asn Ala Ala Leu Ser Arg Ile Met Gly Lys Tyr Gln Leu Ser
182                               675                               680                               685
183 Pro Thr Val Asn Met Pro Gln Asp Asp Thr Val Ile Ile Glu Asp Asp
184                               690                               695                               700
185 Arg Leu Pro Val Leu Pro Pro His Leu Ser Asp Gln Ser Ser Ser Ser
186 705                               710                               715                               720
187 Ser His Asp Asp Val Gly Phe Val Thr Ala Asp Ala Gly Thr Trp Ala
188                               725                               730                               735
189 Lys Ala Ala Ile Ser Asp Ser Ala Asp Cys Ser Leu Ser Pro Asp Val
190                               740                               745                               750
191 Asp Pro Val Leu Ala Phe Gln Arg Glu Gly Phe Gly Arg Gln Ile Ala
192                               755                               760                               765
193 Asp Glu Thr Lys Leu Asn Thr Val Asp Asp Gln Lys Ala Gly Ser Pro
194                               770                               775                               780
195 Ser Arg Asp Val Gly Pro Ser Leu Gly Leu Lys Lys Ser Ser Ser Leu
196 785                               790                               795                               800
197 Glu Ser Leu Gln Thr Ala Val Ala Glu Val Thr Leu Asn Gly Asp Ile
198                               805                               810                               815
199 Pro Phe His Arg Pro Arg Pro Arg Ile Ile Arg Gly Arg Gly Cys Asn
200                               820                               825                               830
201 Glu Ser Phe Arg Ala Ala Ile Asp Lys Ser Tyr Asp Lys Pro Ala Val
202                               835                               840                               845
203 Asp Asp Asp Asp Glu Gly Met Glu Thr Leu Glu Glu Asp Thr Glu Glu

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204      850      855      860
205 Ser Ser Arg Ser Gly Arg Glu Ser Val Ser Thr Ala Ser Asp Gln Pro
206 865      870      875      880
207 Ser His Ser Leu Glu Arg Gln Met Asn Gly Asn Gln Glu Lys Gly Asp
208      885      890      895
209 Lys Thr Asp Arg Lys Lys Asp Lys Thr Gly Lys Glu Lys Lys Lys Asp
210      900      905      910
211 Arg Asp Lys Glu Lys Asp Lys Met Lys Ala Lys Lys Gly Met Leu Lys
212      915      920      925
213 Gly Leu Gly Asp Met Phe Arg Phe Gly Lys His Arg Lys Asp Asp Lys
214      930      935      940
215 Ile Glu Lys Thr Gly Lys Ile Lys Ile Gln Glu Ser Phe Thr Ser Glu
216 945      950      955      960
217 Glu Glu Arg Ile Arg Met Lys Gln Glu Gln Glu Arg Ile Gln Ala Lys
218      965      970      975
219 Thr Arg Glu Phe Arg Glu Arg Gln Ala Arg Glu Arg Asp Tyr Ala Glu
220      980      985      990
221 Ile Gln Asp Phe His Arg Thr Phe Gly Cys Asp Asp Glu Leu Met Tyr
222      995      1000      1005
223 Gly Gly Val Ser Ser Tyr Glu Gly Ser Met Ala Leu Asn Ala Arg Pro
224      1010      1015      1020
225 Gln Ser Pro Arg Glu Gly His Met Met Asp Ala Leu Tyr Ala Gln Val
226 1025      1030      1035      1040
227 Lys Lys Pro Arg Asn Ser Lys Pro Ser Pro Val Asp Ser Asn Arg Ser
228      1045      1050      1055
229 Thr Pro Ser Asn His Asp Arg Ile Gln Arg Leu Arg Gln Glu Phe Gln
230      1060      1065      1070
231 Gln Ala Lys Gln Asp Glu Asp Val Glu Asp Arg Arg Arg Thr Tyr Ser
232      1075      1080      1085
233 Phe Glu Gln Pro Trp Pro Asn Ala Arg Pro Ala Thr Gln Ser Gly Arg
234      1090      1095      1100
235 His Ser Val Ser Val Glu Val Gln Met Gln Arg Gln Arg Gln Glu Glu
236 1105      1110      1115      1120
237 Arg Glu Ser Ser Gln Gln Ala Gln Arg Gln Tyr Ser Ser Leu Pro Arg
238      1125      1130      1135
239 Gln Ser Arg Lys Asn Ala Ser Ser Val Ser Gln Asp Ser Trp Glu Gln
240      1140      1145      1150
241 Asn Tyr Ser Pro Gly Glu Gly Phe Gln Ser Ala Lys Glu Asn Pro Arg
242      1155      1160      1165
243 Tyr Ser Ser Tyr Gln Gly Ser Arg Asn Gly Tyr Leu Gly Gly His Gly
244      1170      1175      1180
245 Phe Asn Ala Arg Val Met Leu Glu Thr Gln Glu Leu Leu Arg Gln Glu
246 1185      1190      1195      1200
247 Gln Arg Arg Lys Glu Gln Gln Met Lys Lys Gln Pro Pro Ser Glu Gly
248      1205      1210      1215
249 Pro Ser Asn Tyr Asp Ser Tyr Lys Lys Val Gln Asp Pro Ser Tyr Ala
250      1220      1225      1230
251 Pro Pro Lys Gly Pro Phe Arg Gln Asp Val Pro Pro Ser Pro Ser Gln
252      1235      1240      1245

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Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:303 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12